

1/13

Fig. 1

A

Selection of candidate SM synthases  
from the animal database

266,504 entries searched (06/02)

1) LPP motif:  $H-\Phi-x_2-D-b-x_2-n-x_3-n$

2) Biochemical function unknown

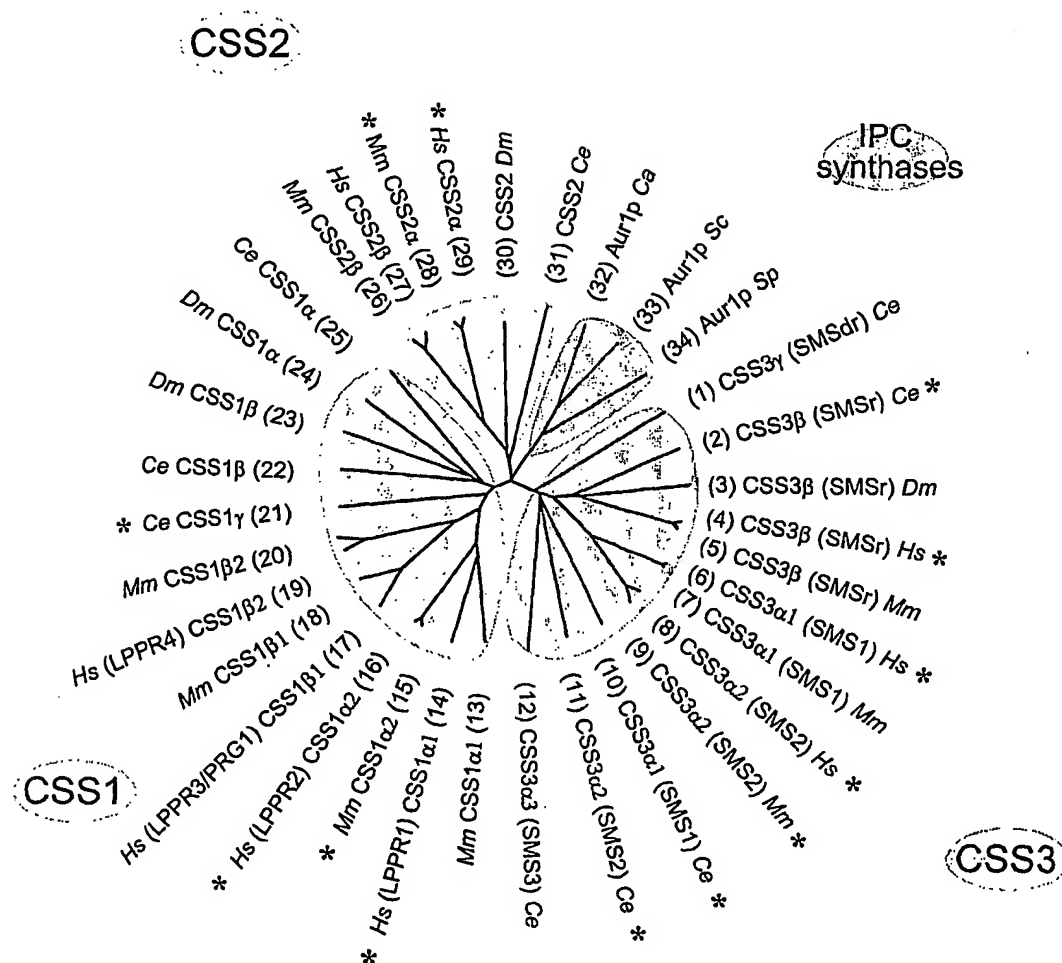
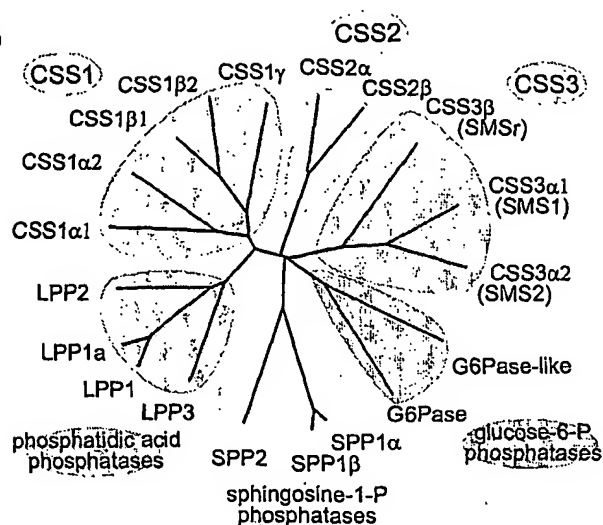
3) No homologues in yeast

BLAST  
search

4) >2 transmembrane domains

31 candidate SM synthase sequences  
human (9), mouse (9), worm (9), fly (4)

B



2/13

Fig. 2

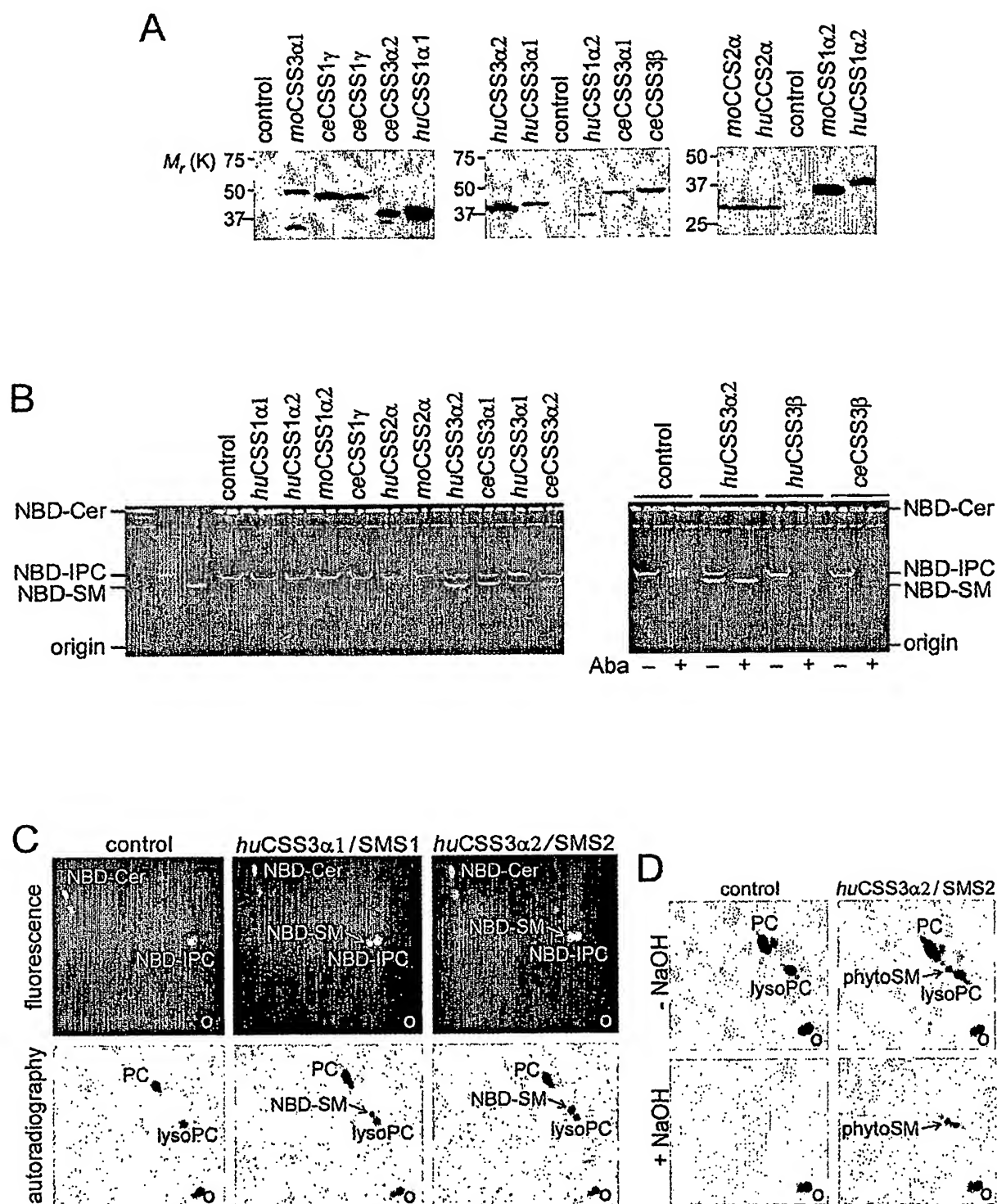


Fig. 3

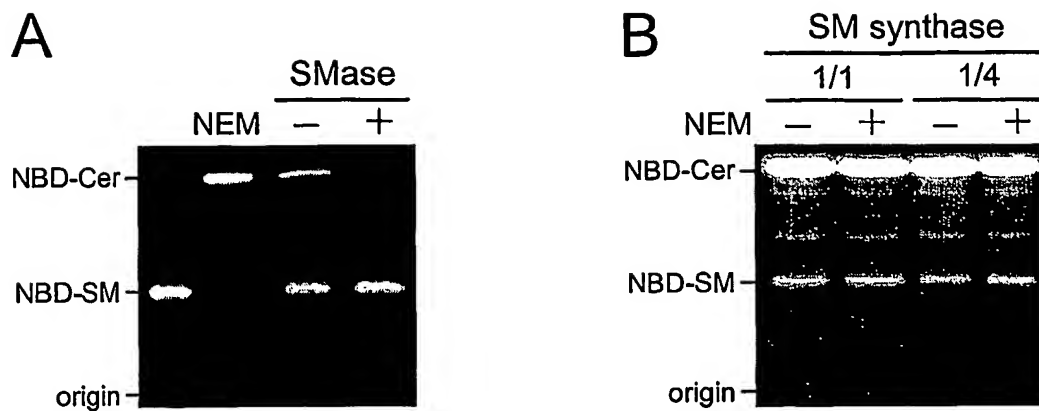
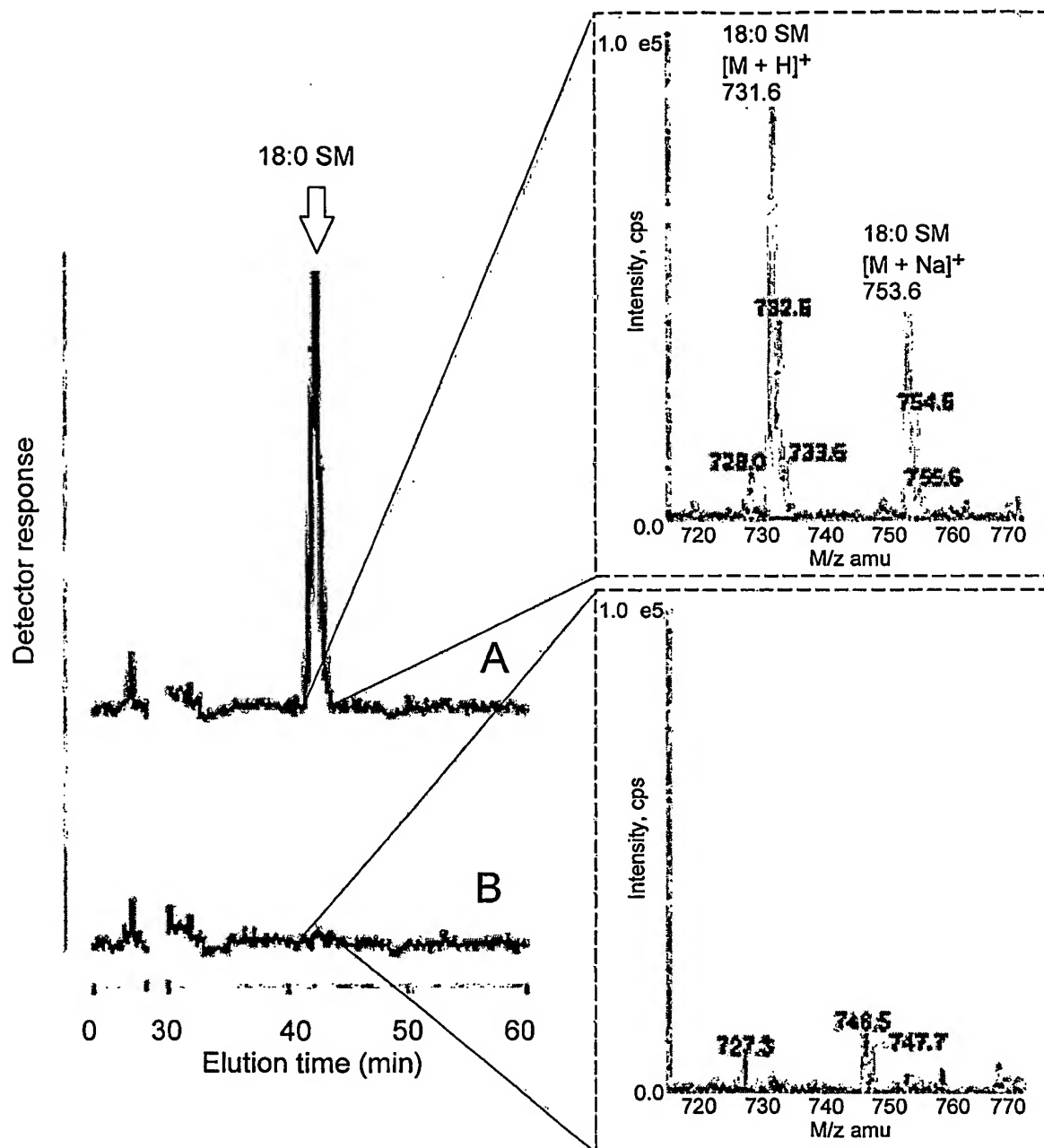
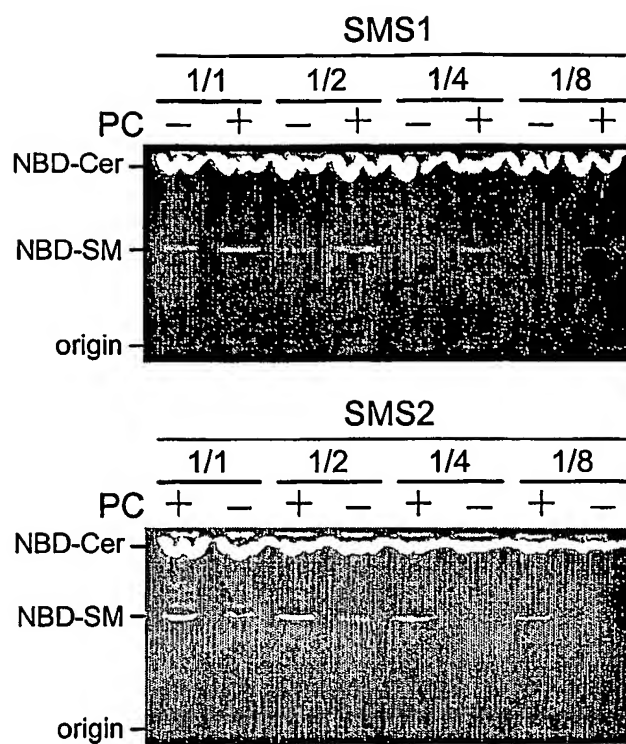


Fig. 4



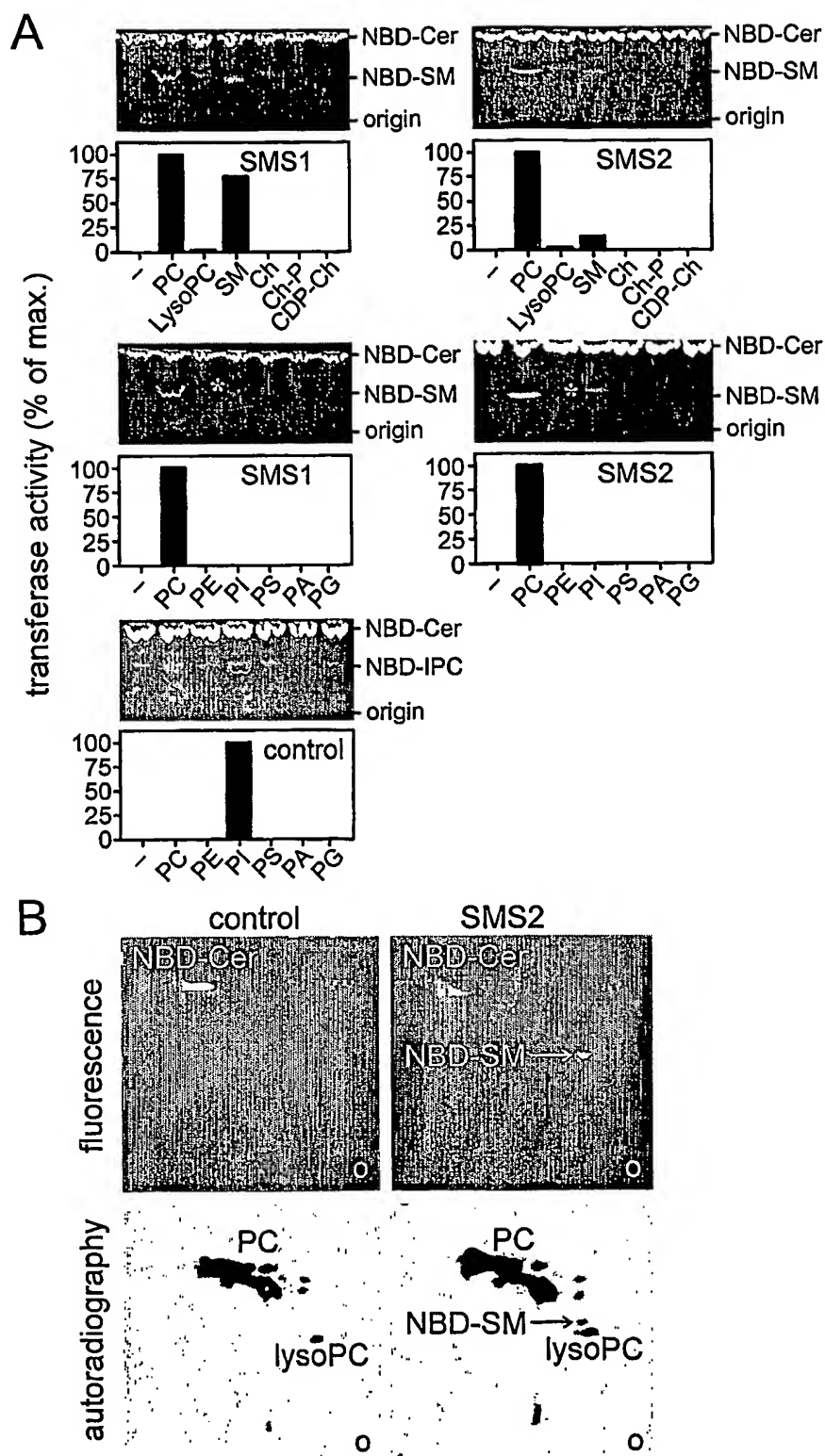
5/13

Fig. 5



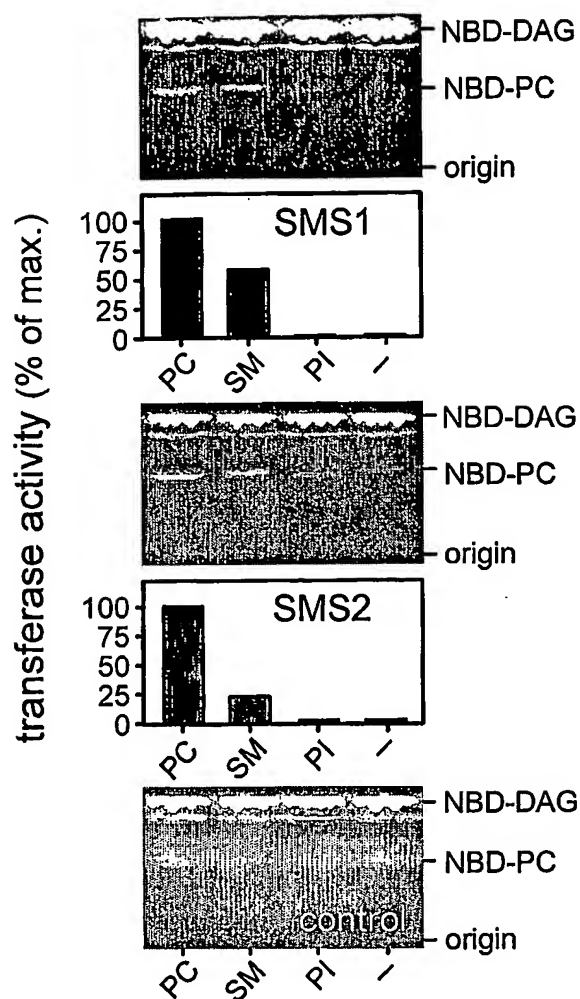
6/13

Fig. 6



7/13

Fig. 7



8/13

Fig. 8

A

Hs SMS1 1 MKEVIVYWSPKKVAADWLEENAMPEYCEPLE--HFTGQDLINLTQEDFKKPPLCRVSSDNG  
Hs SMS2  
Hs SMSr 1 MAGPNQLCLRRWTTKHVAVWLKDEGF FEYVDILCNKHRLDGITLTLTEYDLRSPPLEIKVLGD I

Hs SMS1 58 QRL LDM IETL KMEHH--LEAH--KNGHANGHLN--IGVDIPTPDGSFSIKIKP NG-MPNGYRK-  
Hs SMS2 1 MDI IETAKLEEH--LENQ--PSDPTNTYARPAEPVEEENKNGNGKPKSLSSG-LRKGTKKY  
Hs SMSr 66 KRLMLSVRKLQKIHIDVLEEMGYNSQSPMGSMTPFISALQSTDWLCNGEISHDGDPITD LNSDQ

TM1 -D1-

Hs SMS1 114 -EMIKIPPELERSQYPMEWGKTF LAFYALSCFVLTVMISVVHERVPPKEVQPPLPDTFFDHF  
Hs SMS2 58 PDYIGIAMP TESRNKFPLEWWTGIAFIYAVFNVLVTTVMITVVHERVPPKEVQPPLPDKFFDYI  
Hs SMSr 131 YQYMNKGKNKHSVRRLDP-EYWKTI LSCGYVFI VFGFTSFIMVIVHERVPPDMQTYPPLPDI FLDSV

TM2 D2-TM3

Hs SMS1 178 NRVQWAFSICEINGMILVGLWLTQWLLKYKSIH SRRFCI VGTLYLYRCITMYVTLTPVPGMHF  
Hs SMS2 122 DRVKWAFSVSEINGMILVGLWLTQWLLKYKSIH SRRFCI IGTLYLYRCITMYVTLTPVPGMHF  
Hs SMSr 196 PRTPWAFAMTEVCGMILCYIWLVLVLLHKHRSILLRRLCSLMGTVE LRCFTMFVTSLSVPGQHL

D3 TM4

Hs SMS1 243 NCSPKLF GDWEAQLRRIMKLIAGGGLSITGSHNM CGDYLYSGHTVMTLTLYLF IKEYSPRRLWWY  
Hs SMS2 187 QCAPKLN GDSQAKVQRILRLISGGGLSITGSHI CGD FLFSGHTVTLTLYLF IKEYSPRHFWY  
Hs SMSr 260 QGTGKI YGSVWEKLHRAFAIWSGFGMTLTGVH-TCGDYMFSGHTVVTMLNFFVTETVTPRSWNFL

TM5 D4-TM6

Hs SMS1 309 HWICWLLSVVGIFCILLAH DHYTVDVV VAYYITTRLFWWYHTMANQQLKEASQMNLLARVWWYR  
Hs SMS2 252 HLICWLLSAAGIICILVAHEHYTDV IAYYITTRLFWWYHSMANEKLNKVSSQTNFLSRAWWFP  
Hs SMSr 324 HTLSWVLNLFGIFFFLAAHEHYSTDVF IAYYITTRLFVLYHTLANTR----AYQQSRRARIW-FP

Hs SMS1 373 PFQYFEKNVQGI VPRSYHWPFPWR-VVHLSRQVKYSRLVNDT  
Hs SMS2 317 IFYFFEKNVQGSIPCCESWPLSWPPGCFKSSCKKYSRYQKIGEDNEKST  
Hs SMSr 384 MRSFEKNVNGTVRNEYCWPFESKRAIKRLIG

B

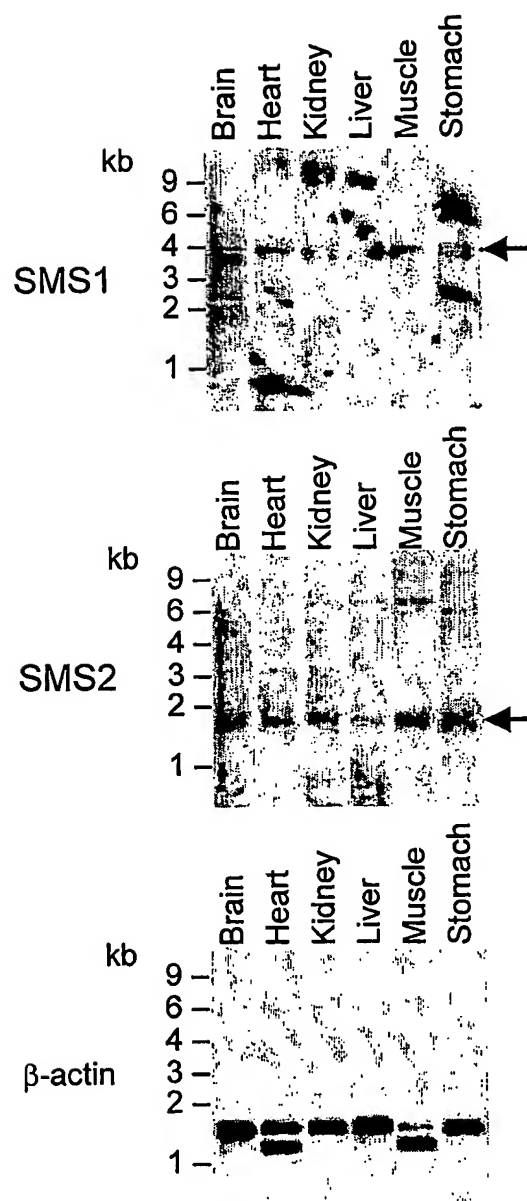
-D1- D2 D3 D4

Hs SMS1 168 PLPD 213 RRFECIVGTLYLYRCITMYVT 277 CGDYLYSGHT 328 HYTVDVV VAYYITTRLFWWYH  
Hs SMS2 112 PLPD 157 RRFECILGTLYLYRCITMYVT 221 CGD FLFSGHT 272 HYTDV I IAYYITTRLFWWYH  
Ce SMS1 175 PLPD 220 RRLCFIGSILYGMRCITMYVT 288 CGDYLYSGHT 339 HYTDVILSYFACTRVFWAYH  
Ce SMS2 88 PLPD 133 RRTFLLGAIMYGLRAVILGVT 202 CGDLMFSGHT 253 HYTMQVLTAYWLTISHVFWSYH  
Ce SMS3 65 SLPD 110 KRNVFCAGTLYAMRSVTLAAT 175 CGD LFSGHT 226 HYTDVVIAYWLSNMVFRMYH  
Pf SMS1 161 PLKD 211 IRI LLLSFIYCI RSEFIYVT 266 CTDLV I SGHT 315 HYTVQVLMGVVFGGSVFLFYH  
Pf SMS2 112 PLSD 161 CRFLYIVGSFYIIRGLLIYVT 216 CADLI VSGHT 265 HYISDVLLGLIFGVFMFSFYH  
Hs SMSr 185 PLPD 230 RRLCSLMGTVLLRCFTMEVT 293 CGDYMFSGHT 344 HYISIDVFIAYYITTRLFVLYH  
Dm SMSr 232 PLPD 277 RRFALAGTVLLRCVTMLIT 350 CGDYMFSGHT 401 HYISIDVFIAYYITSRFLVLYH  
Ce SMSr 214 PLPD 259 RRMFSLLGTVLLRCFTMLIT 322 CGDYMFSGHT 373 HYISIDVFIAYYISSRMFLVLYH  
Ce SMSdr 111 PLPD 183 RRVFFCLAMAYSFRALCYTIF 247 CGDLI VSGHT 298 HYMDIVLCYTVSTRIRMEYH  
consensus PLPD RRxxx b x n x b x x R x x b x b T CGD x b x SGHT HYT b D V x b n x x n n x b F x x YH



9/13

Fig. 10



10/13

Fig. 11

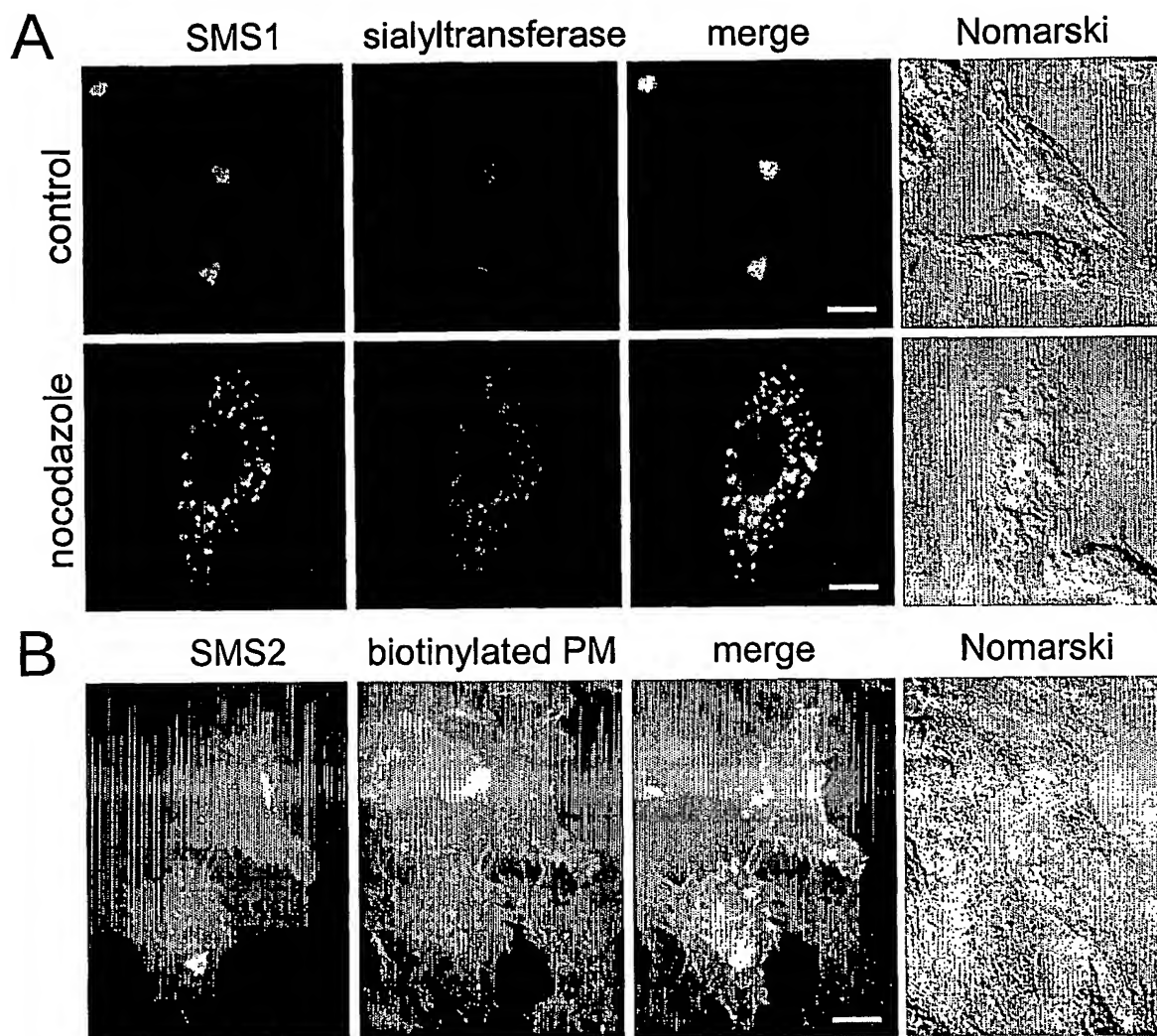
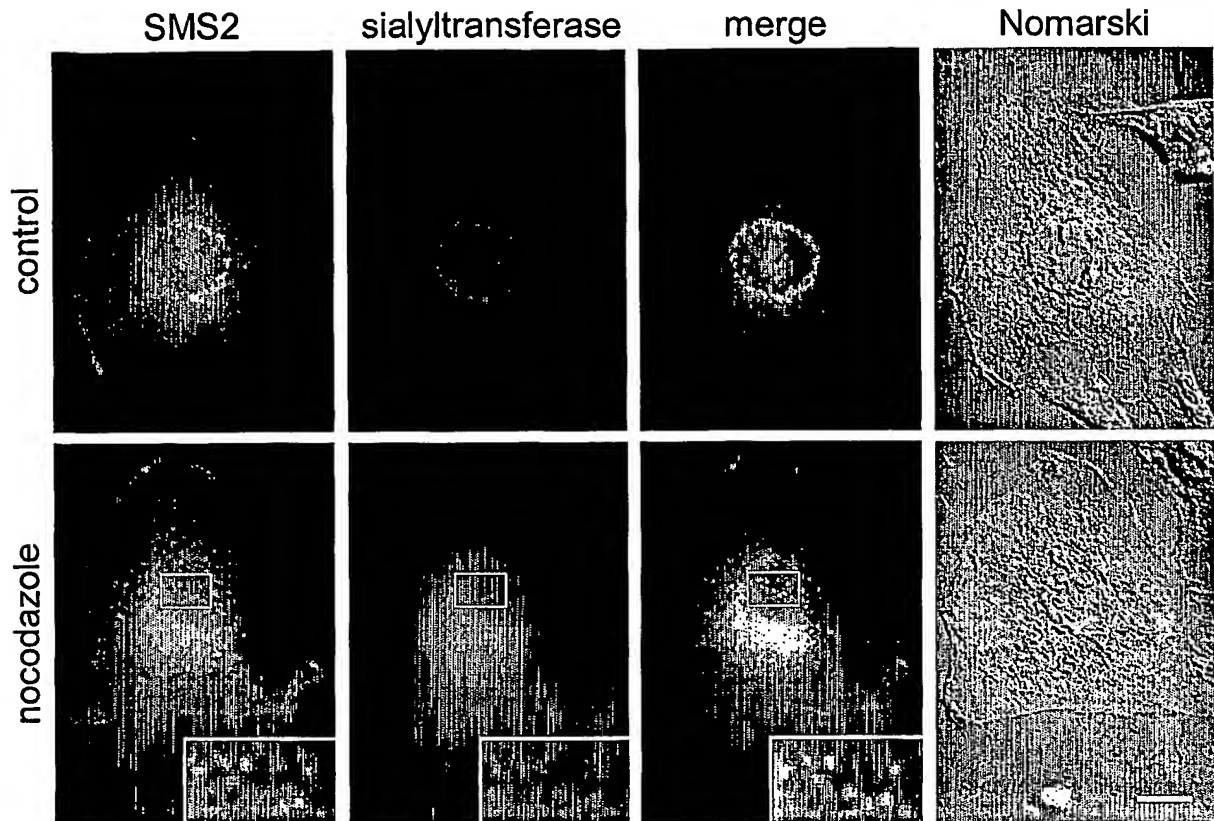
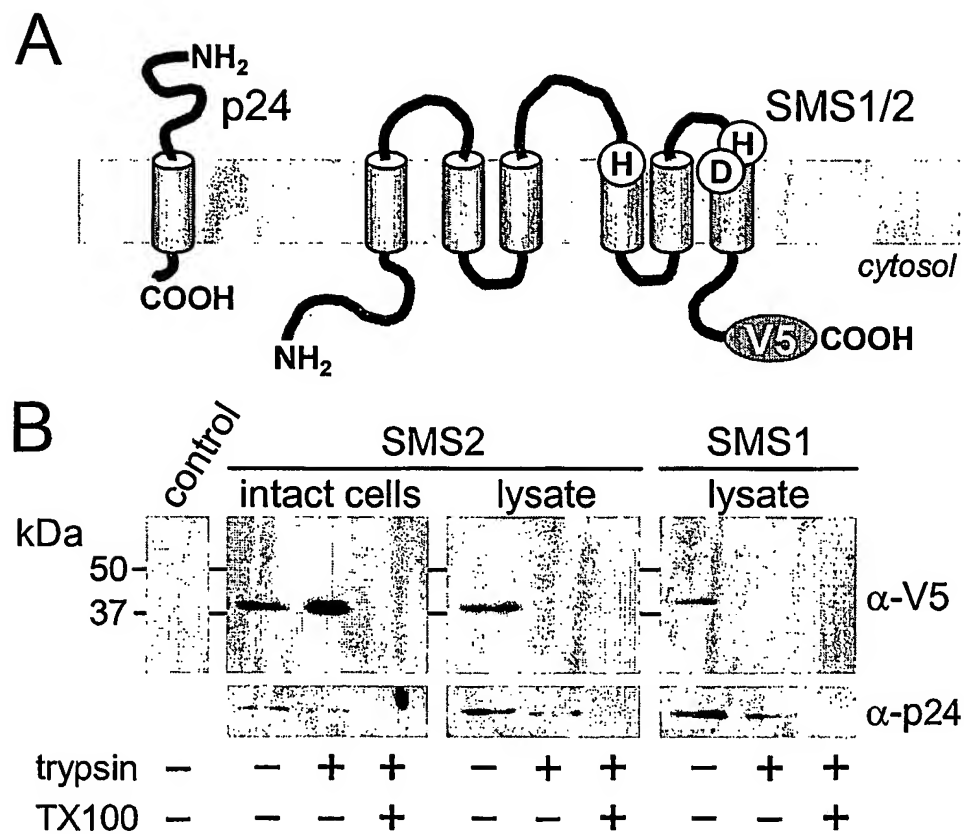


Fig. 12



12/13

Fig. 13



13/13

Fig. 14

